Mini Review

Possible Reasons of High Frequency Transmission of the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-Cov-2)

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Abstract

The ongoing COVID-19 pandemic instigated by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has been the major subject of research in the year 2020. While the genomic characterization and the host immune response have been well-plotted so far, the COVID-19 transmission dynamics remain as an obscure although several research groups have come up with genomic epidemiology and projections of the SARS-CoV-2 transmission potential through mathematical modeling and simulations. The basic reproductive number of the SARS-CoV-2; i.e., the expected number of secondary infection cases spawned by a COVID-19 case, has been noticed to be relatively much higher than those of other recently emerged pathogens including Dengue Virus (DNV), Zika Virus (ZIKV), Chikungunya Virus (CHIKV), etc. as well as compared to the previous versions of coronaviruses including SARS-CoV-1 and the Middle East Respiratory Syndrome coronavirus (MERS-CoV). The current review discussed in short, the possible causes and effects of the transmission dynamics based on the recently published literature, and proposed a simplistic but novel scheme inferring the parameters of SARS-CoV-2 distribution worldwide.

Keywords

COVID-19 Pandemic; Transmission Dynamics; SARS-CoV-2

Introduction

Along with the present COVID-19 pandemic, the shattering of the global public health by several re-emerging viruses especially the dengue virus (DENV), chikungunya virus (CHIKV), Nipah virus (NIV), Ebola virus, etc. has been vigorously noticed for the last three decades **(**1-5**)**. There are true, other dreadful viruses amongst which the respiratory viral infections seem to be persistent for 100 years **(**1**)**. The evolution of the coronaviruses is now very well-known regarding their associated vectors, mode of transmission, epidemiology, genomics, viral reassortment, pathogenesis strategies and preventive care **(**6-10**)**. The most important facet of the studies so far conducted has been noticed through the evasion strategies of the coronaviruses especially of the COVID-19 causing severe acute respiratory syndrome β-coronavirus (SARS-CoV-2) as well as the underlying conditions rendering the COVID-19 severity **(**11-13**)**.

The concomitant efforts for drug designing and vaccine development against SARS-CoV-2 seem to be ineffective; however, the strategy of drug repurposing is somewhat operative in treating the COVID-19 severity **(**14,15**)**.

Compared to the extent of spread and fatal impacts posed by the previous versions of coronaviruses; i.e., SARS-CoV-1 and the Middle East respiratory syndrome coronavirus (MERS), the frequency of spread of SARS-CoV-2 has been noticed to be many-fold higher since its emergence in Wuhan, the known ground zero of the SARS-CoV-2 at the back end of December 2019 **(**6-8**)**. The present review interpreted such high-speed transmission potential of SARS-CoV-2 based on the knowledge accumulated from the recent literature published.

Mutation as a cause of high-frequency transmission of SARS-CoV-2

One interesting trait of the SARS-CoV-2 has been reported which is its ability to proofread the genomes during replication and recombination, thereby rending it heterogeneous and dynamic as well permitting the virus undergoing rapid mutations even as a simulative response towards the host protective immunity in the individuals of diverse races, ages, and the underlying medical conditions **(**8, 13, 16**)**.

As reported earlier by Ferron et al. (2018), the frequency mutation within SARS-CoV-2 could result in diverse variants in a short time scale which has been later proven correct, as the recent genotyping analysis has revealed several random mutations (or by the host immune system surveillance inducing the viral response depending on the viral fitness) in the genes encoding the viral spike (S) protein (more than 1000 mutations), nucleocapsid (N) protein (more than 500 mutations), envelope (E) protein (more than 50 mutations), main- and the papain-like protease (approximately 400 mutations), endoribonuclease (NendoU) protein (more than 250 mutations) and the RNA dependent RNA polymerase (RdRp) with more than 600 mutations **(**8, 16-18**)**. Indeed, as the SARS-CoV-2 spread faster and wider, the possibility of mutation gets more frequent and diverse **(**8**)**.

The work by Wang et al., 2020 derived the occurrence of 8309 single mutations in 15140 SARS-CoV-2 isolates based on which they further classified and tracked the geographical distributions of those genotypes, and they concluded (utilizing clustering the variants through the Elbow method in the K-means clustering algorithm) that the SARS-CoV-2 genotypes which can be represented as single nucleotide polymorphism (SNP) variants are now clustered as six groups all over the world **(**8**)**.

Seasonal variation influencing the COVID-19 severity

Seasonal variation has been reported to influence the SARS-CoV-2 transmission according to different geographic locations **(**19**)**. Low transmission in summer followed by recurrent wintertime outbreaks; i.e., increased wintertime transmissibility appears to be likely as evident by 10-fold increased positive tests within December-April compared to July-September **(**19, 20**)**. The basic reproduction number (R_0, the average number of new infections per infected SARS-CoV-2 case), an epidemic tool for the measurement of the transmission potential, has been estimated to be approximately 2 to 3 and has been noticed to be governed by the environmental conditions like climate **(**7, 19**)**.

Earlier it has been reported that a value of R_0 less than 1 is suggestive of the self-limiting trait of the pathogen; and therefore, the high R0 for SARS-CoV-2 indicative of high pandemic potential **(**7, 20-22**)**. However, the extensive analysis of the climatic zones, epidemic forecasting, geographical distribution, and the weather conditions revealed that along with a high R_0 value, the COVID-19 lethality tends to increase by 4 times at low temperatures (4-12 ^{o}C) with a relative humidity of 60-80% **(**23**)**.

Mathematical models to analyze the COVID-19 severity

This is to be noted that such analysis and the possible predictions of the COVID-19 pandemic (such as the geographical distribution by country and territory together with the most exposed regions to the COVID-19 pandemic, derivation of the daily mean temperature and humidity about the number of COVID-19 cases, the Winter-Spring-Summer-Autumn isotherm maps, modeling of the epidemic curve, etc.) have been conducted by several mathematical models of epidemics **(**7, 20, 24**)**. In addition to the R_0 value as stated earlier, deducing the

(1) effective reproductive number represented by R (secondary cases induced by the original infectious case after the epidemic initiates),
(2) exposure frequency represented by k,
(3) the infection probability per exposure as expressed by β_0, and
(4) the average recovery time represented by Ti,
(5) deducing the rate at which an infected individual infects a susceptible one as expressed by $\beta(t)$,
(6) detection of the inverse latency time represented by μ,
(7) detection of the recovery rate as expressed by ν,

(8) determining the population turn-over rate represented by b, are also needed to analyze the pandemic potential **(**7, 20, 24**)**.

Such mathematical investigation (mostly using the SIR model; i.e., susceptibility, infectivity and recovery) has shown the progress of an epidemic in a homogeneous population as well as pointed on the threshold density of population in a relative aspect of the frequency of infectivity, recovery and death rates **(**24**)**. Besides, the notable indication of the fact that even a small increase of the infectivity rate may instigate a huge epidemic derived through such mathematical modeling is of large interest of the scientists working against COVID-19 having both latency time and the incubation time/infectious period of around 5 days **(**20, 24**)**.

Host protective immunity, the cross-immunity, and the recurring outbreaks of COVID-19

The possible cross-immunity between SARS-CoV-2 and the HCoV-OC43 and HCoV-HKU1, (two other coronaviruses along with SARS-CoV-2 and SARS-CoV-1 and MERS-CoV existing within the b-coronavirus family), has been suggested to influence the post-pandemic transmission of SARS-CoV-2 **(**25**)**. It is stipulated that such cross-immunity may lower the possibility of SARS-CoV-2 outbreaks although there exists an opposite idea that the antibody-dependent enhancement (ADE) stimulated by the prior infection may boost the predisposition towards the COVID-19 severity **(**19, 25**)**. Also, if the immunity to SARS-CoV-2 declines, the recurrent wintertime outbreaks are very much likely to commence in the future **(**19**)**.

Moreover, it is to be noted that while the short-term immunity is known to support the commencement of annual SARS-CoV-2 outbreaks, the long-term immunity (lasting only for 2 years, consistently leading to the exclusion of the virus) has also been reported to bolster the biyearly outbreaks **(**19**)**. It's also interesting to note that the mild cross-immunity (estimated as much as 30%) from HCoV-OC43 and HCoV-HKU1 has been predicted to eliminate the SARS-CoV-2 transmission for up to three years **(**19**)**. Thus, cross-immunity may play a vital role in SARS-CoV-2 transmission or its elimination.

In fine, it must be noted that the estimation of clinical severity of SARS-CoV-2 infection with an R0 value of more than 2 (principally, the overall symptomatic case fatality risk; i.e., the probability of dying after developing symptoms) during a pandemic is a public health urgency; and it requires the accurate adjustment of ascertainment rate and the delay between symptoms

onset and death **(**26**)**. Indeed, a high basic reproductive number imparts SARS-CoV-2 the ability of homogeneous mixing and mass action dynamics which in turn results in the COVID-19 severity worldwide as is currently noticed around the world **(**7, 26**)**. A simplified scheme of the SARS-CoV-2 dynamics has been presented in **Figure1** showing the viral transmission influencing parameters along with the mathematical variables as described above**.**

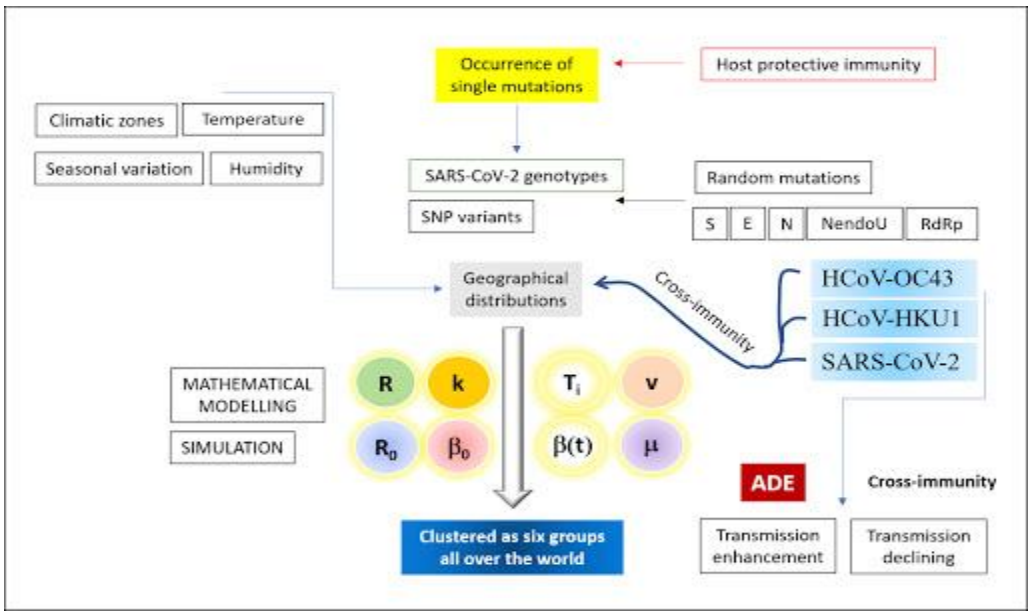

Figure 1: A simplified scheme of SARS-CoV-2 transmission dynamics involving the random mutations, host protective immunity, cross immunity between other coronaviruses, seasonal impact, and finally, the mathematical modelling and simulation. Details are explained in the text.

Conclusion

Chasing and investigation of COVID-19 dynamics through the study of COVID-19 genomic epidemiology as well as the SARS-CoV-2 transmission are of utmost significance for remediating the COVID-19 severity. Such an approach would help design the appropriate drugs besides the current practice of drug repurposing as well as to develop vaccines maintaining the geographical specificity.

Conflict of interest

Authors have declared that they no conflict of interest.

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References

1.Noor R, Maniha SM. "A brief Outline of Respiratory Viral Disease Outbreaks: 1889 – Till Date on the Public Health Perspectives". VirusDisease 2020. DOI: 10.1007/s13337-020-00628-5.

2.Noor R. "Re-emergence of dengue virus in Bangladesh: Current fatality and the required knowledge". Tzu Chi Med J 2020; 32(3): 227–233.

3.Noor R., Ahmed T. Zika virus: "Epidemiological study and its association with public health risk". Journal of Infection and Public Health 2018; 11(5): 611-616.

4.Noor R. and Maniha SM. "Chikungunya Virus (CHIKV) Infection and the Protective Immunity: A Narrative Review". EC Emergency Medicine and Critical Care 2020: 4(3): 1-10.

5.Afrough B, Dowall S, Hewson R. "Emerging viruses and current strategies for vaccine intervention". Clin Exp Immunol. 2019;196(2):157-166.

6.Asaduzzaman SAI, Zakaria A, Kheya IS, Fahad N, Sikandar YB, Noor R. "A comparative study between the severe acute respiratory syndrome-coronavirus-2, severe acute respiratory syndrome coronavirus, and the Middle East respiratory syndrome coronavirus". Biomed Biotechnol Res J 2020; 4: S65-74.

7.Fahad N, Asaduzzaman SAI, Zakaria A, Noor R. "A Brief Report on the Transmission Dynamics of the Severe Acute Respiratory Coronavirus-2 (SARS-CoV-2)". EC Emergency Medicine and Critical Care 2020; 4(9): 56-59.

8.Wang R, Hozumi Y, Yin C, Wei GW. "Decoding SARS-CoV-2 Transmission and Evolution and Ramifications for COVID-19 Diagnosis, Vaccine, and Medicine". J Chem Inf Model. 2020:acs.jcim.0c00501. doi: 10.1021/acs.jcim.0c00501.

9.Sikandar YB, Maniha MM, Taaseen WI, Noor R. "Characterization of the Host Receptor Binding by the Severe Acute Respiratory Coronavirus-2 (SARSCoV-2), SARS-CoV and the Middle East Respiratory Syndrome coronavirus (MERS-CoV)". EC Microbiology 2020; 16(10): 24-27.

10.Fatima K, Noor R. “Coronavirus (CoV) Pathogenesis and Host Immunology”. EC Microbiology 2020; 16(10): 28- 30.

11.Maniha SM, Haque SN, Akhter M, Noor R. “Ongoing COVID-19 Pandemics by the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) and the Host Protective Immunity Response: A Simple Outline”. EC Emergency Medicine and Critical Care 2020; 4(6): 103-108.

12.Kheya IS, Sikandar YB, Fahad N, Asaduzzaman SAI, Zakaria A, Noor R. “Orchestration of Host Immunity with Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Infection”. EC Microbiology 2020; 16(10): 57-61.

13.Noor R. “Obesity and Diabetes as the Predisposing Medical Risk Factors for the COVID-19 Severity”. J Bacteriol Mycol. 2020; 7(7): 1154.

14.Noor R. “Antiviral drugs against severe acute respiratory syndrome coronavirus 2 infection triggering the coronavirus disease-19 pandemic”. Tzu Chi Med J 2020; DOI: 10.4103/tcmj.tcmj_100_20.

15.Taaseen WI, Noor R. “Drug Designing and Repositioning against Severe Acute Respiratory Coronavirus 2 (SARS-Cov-2) through Computational Simulation: Current Progress and Hopes”. J Microbiol Biotechnol 2020, 5(3): 000168.

16.Ferron F, Subissi L, Silveira De Morais AT, Le N TT, Sevajol M, Gluais L, Decroly E, Vonrhein C, Bricogne G, Canard B, Imbert I. “Structural and molecular basis of mismatch correction and ribavirin excision from coronavirus RNA”. Proc. Natl. Acad. Sci. U. S. A. 2018, 115 (2), E162–E171. 10.1073/pnas.1718806115.

17.Tang X, Wu C, Li X, Song Y, Yao X, Wu X, Duan Y, Zhang H, Wang Y, Qian Z, Cui J, Lu J. “On the origin and continuing evolution of SARS-CoV-2. Nat”. Sci. Rev. 2020, 7, 1012.10.1093/nsr/nwaa036.

18.Yin C. Genotyping coronavirus SARS-CoV-2: “methods and implications”. Genomics 2020, 10.1016/j.ygeno.2020.04.016.

19.Kissler SM, Tedijanto C, Goldstein E, Grad YH, Lipsitch M. "Projecting the transmission dynamics of SARS-CoV-2 through the postpandemic period. Science". 2020 May 22;368(6493):860-868.

20.Neher R. A., Dyrdak R., Druelle V., Hodcroft E. B., Albert J., "Potential impact of seasonal forcing on a SARS-CoV-2 pandemic". Swiss Med. Wkly. 150, w20224 (2020). 10.4414/smw.2020.20224.

21.Fang Y, Nie Y, Penny M. "Transmission dynamics of the COVID-19 outbreak and effectiveness of government interventions: A data-driven analysis". J Med Virol. 2020; 92(6):645-659.

22.Zhao S, Lin Q, Ran J, Musa SS, Yang G, Wang W, Lou Y, Gao D, Yang L, He D, Wang MH. "Preliminary estimation of the basic reproduction number of novel coronavirus (2019-nCoV) in China, from 2019 to 2020: A data-driven analysis in the early phase of the outbreak". Int J Infect Dis. 2020; 92:214-217.

23.Scafetta N. "Distribution of the SARS-CoV-2 Pandemic and Its Monthly Forecast Based on Seasonal Climate Patterns". Int J Environ Res Public Health. 2020;17(10):3493.

24.Kermack WO, McKendrick AG. "Contributions to the mathematical theory of epidemics—I". 1927. Bull Math Biol. 1991;53(1-2):33–55.

25.Tetro JA. "Is COVID-19 receiving ADE from other coronaviruses? Microbes Infect".2020; 22: 72–73.

26.Wu JT, Leung K, Bushman M, Kishore N, Niehus R, de Salazar PM, Cowling BJ, Lipsitch M, Leung GM. "Estimating clinical severity of COVID-19 from the transmission dynamics in Wuhan, China". Nat Med. 2020;26(4):506-510.

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